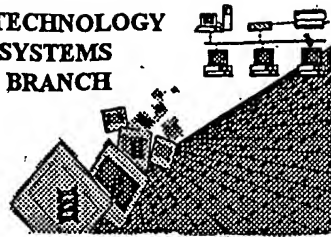


## RAW SEQUENCE LISTING ERROR REPORT

BIOTECHNOLOGY  
SYSTEMS  
BRANCH



0300  
7/2

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number:

10/045,594A

Source:

OPE

Date Processed by STIC:

4/12/02

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: [patin21help@uspto.gov](mailto:patin21help@uspto.gov) or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: [patin3help@uspto.gov](mailto:patin3help@uspto.gov) or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER  
VERSION 3.1 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND  
TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<<http://www.uspto.gov/ebc/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:  
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7<sup>th</sup> Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202  
Or  
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service, or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

# Raw Sequence Listing Error Summary

01PE

ERROR DETECTED	SUGGESTED CORRECTION	SERIAL NUMBER: 10/045,594A
ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE		
1 ____ Wrapped Nucleics Wrapped Aminos	The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."	
2 ____ Invalid Line Length	The rules require that a line not exceed 72 characters in length. This includes white spaces.	
3 ____ Misaligned Amino Numbering	The numbering under each 5 <sup>th</sup> amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.	
4 ____ Non-ASCII	The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.	
5 ____ Variable Length	Sequence(s) ____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.	
6 ____ PatentIn 2.0 "bug"	A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.	
7 ____ Skipped Sequences (OLD RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence: (2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) (i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading) (xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown) This sequence is intentionally skipped  Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.	
8 ____ Skipped Sequences (NEW RULES)	Sequence(s) ____ missing. If intentional, please insert the following lines for each skipped sequence. <210> sequence id number <400> sequence id number 000	
9 <input checked="" type="checkbox"/> Use of n's or Xaa's (NEW RULES)	Use of n's and/or Xaa's have been detected in the Sequence Listing. Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present. In <220> to <223> section, please explain location of n or Xaa; and which residue n or Xaa represents.	
10 ____ Invalid <213> Response	Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence	
11 ____ Use of <220>	Sequence(s) ____ missing the <220> "Feature" and associated numeric identifiers and responses. Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section. (See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)	
12 ____ PatentIn 2.0 "bug"	Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.	
13 ____ Misuse of n	n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.	



**Does Not Comply**  
**Corrected Diskette Needed**

OIPE

## RAW SEQUENCE LISTING

DATE: 04/12/2002

PATENT APPLICATION: US/10/045,594A

TIME: 13:46:31

Input Set : A:\UTSD729US.APP

Output Set: N:\CRF3\04122002\J045594A.raw

3 <110> APPLICANT: OLSON, ERIC  
4 FREY, NORBERT  
6 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS RELATING TO MUSCLE SPECIFIC  
7 CALCINEURIN ASSOCIATED PROTEIN (CAP)  
9 <130> FILE REFERENCE: UTSD:729US  
11 <140> CURRENT APPLICATION NUMBER: 10/045,594A  
12 <141> CURRENT FILING DATE: 2001-11-07  
14 <150> PRIOR APPLICATION NUMBER: 60/246,629  
15 <151> PRIOR FILING DATE: 2000-11-07  
17 <160> NUMBER OF SEQ ID NOS: 12  
19 <170> SOFTWARE: PatentIn Ver. 2.1

## ERRORED SEQUENCES

223 <210> SEQ ID NO: 5  
224 <211> LENGTH: 1261  
225 <212> TYPE: DNA  
226 <213> ORGANISM: Homo sapiens  
228 <400> SEQUENCE: 5  
229 cggtcacagc agctcagtc tccaaagctg ctggacccca gggagagctg accactgccc 60  
230 gaggcagccg ctgaatccac ctccacaatg cgcctctcag gaaccccgcc ccctaataag 120  
231 aagaggaaat ccagcaagct gatcatggaa ctcaactggag gtggacagga gagctcaggc 180  
232 ttgaacctgg gcaaaaagat cagtgtccca agggatgtga tgttgaggga actgtcgtg 240  
233 cttaccaacc ggggctccaa gatgttcaaa ctgcgcgaga tgagggtgga gaagtttatt 300  
234 tatgagaacc accctgatgt tttctctgac agctcaatgg atcacttcca gaagttcctt 360  
235 ccaacagtgg ggggacagct gggcacagct ggtcagggat tctcatacag caagagcaac 420  
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239 ggcggagaag gaaaacatat cactgtgttc aagacctata tttcccatg ggagcgagcc 660  
240 atgggggttg acccccagca aaaaatggaa ctggcattg acctgctggc ctatggggcc 720  
241 aaagctgaac ttcccaaata taagtcttcc aacaggacgg caatgcccta tggtgatat 780  
242 gagaaggcct ccaaacgcat gaccttccag atgcccaagt ttgacctggg gcccttgctg 840  
243 agtgaacccc tggctcctcta caacccaaac ctctccaaca ggccttcttt caatcgaaac 900  
244 cctattccct ggctgagctc tggggagcct gtagactaca acgtggatat tggcatcccc 960  
245 ttggatggag aaacagagga gctgtgaggt gtttctcct ctgatttgca tcatttcccc 1020  
246 tctctggctc caatttgag agggaatgct gagcagatag ccccatgtgt taatccagta 1080  
247 tccttatggg aatggaggga aaaaggagag atctaccttt ccctccttta ctccaagtcc 1140  
248 ccactccacg catccttcc cccaactca gagctccctt tctacttgct ccatatggaa 1200  
E--> 249 cctgctcggt tatggaattt ntctgccacc agtaacagtc aataaacttc aaggaaaatg 1260  
250 a 1261

→ requires explanation for n. seq error  
summary sheet item 9

VERIFICATION SUMMARY

DATE: 04/12/2002

PATENT APPLICATION: US/10/045,594A

TIME: 13:46:32

Input Set : A:\UTSD729US.APP

Output Set: N:\CRF3\04122002\J045594A.raw

L:249 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:5